OM protein - protein search, using sw model

Run on: December 19, 2002, 15:00:53 ; Search time 18 Seconds
(without alignments)
2143.388 Million cell updates/sec

Title: US-08-813-323B-1
Perfect score: 2994
Sequence: 1 MESSKKMDAAGTLQPNPPLK.....IKDDTIFIKVIVDTSDLPDP 567

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 245176 seqs, 68044064 residues

Total number of hits satisfying chosen parameters: 245176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	837.5	28.0	501	6	US-10-283-500-4	Sequence 4, Appli
2	688.5	23.0	519	5	US-09-724-676-53797	Sequence 53797, A
3	688.5	23.0	519	5	US-09-724-676A-53797	Sequence 53797, A
4	682.5	22.8	308	5	US-09-724-676-84446	Sequence 84446, A
5	682.5	22.8	308	5	US-09-724-676A-84446	Sequence 84446, A
6	652.5	21.8	536	5	US-09-724-676-53796	Sequence 53796, A
7	652.5	21.8	536	5	US-09-724-676A-53796	Sequence 53796, A
8	640	21.4	409	6	US-10-283-500-2	Sequence 2, Appli
9	560.5	18.7	470	7	US-60-423-586-89	Sequence 89, Appl
10	560.5	18.7	470	7	US-60-427-194-89	Sequence 89, Appl
11	259	8.7	46	5	US-09-716-536-10	Sequence 10, Appl
12	205.5	6.9	600	6	US-10-197-666A-120	Sequence 120, App
13	203	6.8	641	6	US-10-197-666A-112	Sequence 112, App
14	203	6.8	670	6	US-10-197-666A-150	Sequence 150, App
15	202	6.7	631	6	US-10-197-666A-116	Sequence 116, App
16	200	6.7	631	6	US-10-197-666A-144	Sequence 144, App
17	199	6.6	670	6	US-10-197-666A-114	Sequence 114, App
18	186.5	6.2	72	6	US-10-203-138A-11026	Sequence 11026, A
19	179	6.0	59	5	US-09-724-676-84447	Sequence 84447, A
20	179	6.0	59	5	US-09-724-676A-84447	Sequence 84447, A
21	175	5.8	667	6	US-10-197-666A-118	Sequence 118, App
22	147	4.9	2106	5	US-09-724-676-85182	Sequence 85182, A
23	147	4.9	2106	5	US-09-724-676A-85182	Sequence 85182, A
24	147	4.9	2193	5	US-09-724-676-85181	Sequence 85181, A
25	147	4.9	2193	5	US-09-724-676A-85181	Sequence 85181, A
26	147	4.9	2228	5	US-09-724-676-85180	Sequence 85180, A
27	147	4.9	2228	5	US-09-724-676A-85180	Sequence 85180, A
28	147	4.9	2230	5	US-09-724-676-85179	Sequence 85179, A
29	147	4.9	2230	5	US-09-724-676A-85179	Sequence 85179, A
30	147	4.9	3117	5	US-09-724-676-74707	Sequence 74707, A
31	147	4.9	3117	5	US-09-724-676A-74707	Sequence 74707, A
32	147	4.9	3213	5	US-09-724-676-74706	Sequence 74706, A
33	147	4.9	3213	5	US-09-724-676A-74706	Sequence 74706, A
34	146.5	4.9	1816	6	US-10-299-058-2	Sequence 2, Appli
35	146.5	4.9	1816	6	US-10-299-058-4	Sequence 4, Appli
36	144.5	4.8	987	5	US-09-724-676-85178	Sequence 85178, A
37	144.5	4.8	987	5	US-09-724-676A-85178	Sequence 85178, A
38	144.5	4.8	1074	5	US-09-724-676-85177	Sequence 85177, A
39	144.5	4.8	1074	5	US-09-724-676A-85177	Sequence 85177, A
40	144.5	4.8	1109	5	US-09-724-676-85175	Sequence 85175, A
41	144.5	4.8	1109	5	US-09-724-676-85176	Sequence 85176, A
42	144.5	4.8	1109	5	US-09-724-676A-85175	Sequence 85175, A
43	144.5	4.8	1109	5	US-09-724-676A-85176	Sequence 85176, A
44	144.5	4.8	1111	5	US-09-724-676-85173	Sequence 85173, A
45	144.5	4.8	1111	5	US-09-724-676-85174	Sequence 85174, A

ALIGNMENTS

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RESULT 1
US-10-283-500-4
; Sequence 4, Application US/10283500
;   GENERAL INFORMATION:
;        APPLICANT: Goeddel, David V.
;                   Rothe. Mike
;        TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
;        NUMBER OF SEQUENCES: 59
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/283,500
;             FILING DATE: 30-Oct-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/779,599
;             FILING DATE: 07-Jan-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dreger, Ginger R.
;             REGISTRATION NUMBER: 33,055
;             REFERENCE/DOCKET NUMBER: P0897C2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-3216
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 501 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-283-500-4

  Query Match             28.0%;  Score 837.5;  DB 6;  Length 501;
  Best Local Similarity   33.5%;  Pred. No. 4.7e-71;
  Matches  194;  Conservative   88;  Mismatches  198;  Indels   99;  Gaps   16;

Qy       7 MDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKT-VEDKYKCEKCRLVLCNPKQT 65
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Db      1 MAAASVTSPGSLELLQP------------GFSKTLLGTRLEAKYLCSACKNILRRPFQA 47

Qy     66 ECGHRFCESCMAALLSSSSPKCTAC------QESII---KDKVFKDNCCKREILALQVYC 116
Db     48 QCGHRYCSFCLTSILSSGPQNCAACVYEGLYEEGISILESSSAFPDNAARREVESLPAVC 107

Qy    117 RNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATC 176
Db    108 PND--GCTWKGTLKEYESCHEGLCPFLLTEC--PACKGLVRLSEKEHHTEQECPKRSLSC 163

Qy    177 SHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRY 236
Db    164 QHCRAPCSHVDLEVHYEV-CPKFPLTC-DGCGKKKIPRETFQDHVRACSKCRVLCRFHTV 221

Qy    237 GCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVS----------LLQNESVEKNKS 286
Db    222 GCSEMVETENLQDHELQRLREHLALL--LSSFLEAQASPGTLNQVGPELLQRCQILEQK- 278

Qy    287 IQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEA 346
Db    279 IATFENIVCVLNREVER--------------VAVTAEACSRQHRLDQD----------- 312

Qy    347 DSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQ 406
Db    313 -----KIEALSNKVQQLE----------------------RSIGLKDLAMADLEQKVS 343

Qy    407 VLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGK 466
Db    344 ELEVSTYDGVFIWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGR 403

Qy    467 GTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGE 526
Db    404 GTHLSLFFVVMKGPNDALLQWPFNQKVTLMLLDH-NNREHVIDAFRPDVTSSSFQRPVSD 462

Qy    527 MNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDTSDL 564
Db    463 MNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 501
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RESULT 2
US-09-724-676-53797
; Sequence 53797, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53797
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-53797

Query Match 23.0%; Score 688.5; DB 5; Length 519;
Best Local Similarity 31.9%; Pred. No. 6.6e-57;
Matches 169; Conservative 89; Mismatches 174; Indels 97; Gaps 19;

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Qy     62 PKQTECGHRFCESCMAALLSSSSPKCTAC-QESIIKDKV--------FKDNCCKREILAL 112
Db     62 PFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARKGVESL 121

Qy    113 QVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRAD---CKEKVLRKDLRDHVEKAC 169
Db    122 PAVCPSD--GCTWKGTLKEY-----ESCHEGRCPLMLTECPACKGLVRLGEKERHLEHEC 174

Qy    170 KYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS 229
Db    175 PERSLSCRHCRAPCCGADVKAHHEV-CPKFPLTC-DGCGKKKIPREKFQDHVKTCGKCRV 232

Qy    230 TCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK----------VSLLQ 277
Db    233 PCRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQ 288

Qy    278 N-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEI 336
Db    289 RCESLEKKTA--TFENIVCVLNREVER----------------VAMTAEACS------ 322

Qy    337 RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDI 396
Db    323 ---RQHRLDQD----KIEALSSKVQQLE----------------------RSIGLKDL 351

Qy    397 RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR 456
Db    352 AMADLEQKVRPFQAQCGHRYCSFCLASILRKLQEAVAGRIPAIFSPAFYTSRYGYKMCLR 411

Qy    457 VYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPN 516
Db    412 IYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVT 470

Qy    517 SSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDTSDL 564
Db    471 SSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 519
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RESULT 3
US-09-724-676A-53797
; Sequence 53797, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53797
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-53797

Query Match 23.0%; Score 688.5; DB 5; Length 519;
Best Local Similarity 31.9%; Pred. No. 6.6e-57;
Matches 169; Conservative 89; Mismatches 174; Indels 97; Gaps 19;

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Qy     62 PKQTECGHRFCESCMAALLSSSSPKCTAC-QESIIKDKV--------FKDNCCKREILAL 112
Db     62 PFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARKGVESL 121

Qy    113 QVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRAD---CKEKVLRKDLRDHVEKAC 169
Db    122 PAVCPSD--GCTWKGTLKEY-----ESCHEGRCPLMLTECPACKGLVRLGEKERHLEHEC 174

Qy    170 KYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS 229
Db    175 PERSLSCRHCRAPCCGADVKAHHEV-CPKFPLTC-DGCGKKKIPREKFQDHVKTCGKCRV 232

Qy    230 TCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK----------VSLLQ 277
Db    233 PCRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQ 288

Qy    278 N-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEI 336
Db    289 RCESLEKKTA--TFENIVCVLNREVER----------------VAMTAEACS------ 322

Qy    337 RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDI 396
Db    323 ---RQHRLDQD----KIEALSSKVQQLE----------------------RSIGLKDL 351

Qy    397 RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR 456
Db    352 AMADLEQKVRPFQAQCGHRYCSFCLASILRKLQEAVAGRIPAIFSPAFYTSRYGYKMCLR 411
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Qy    457 VYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPN 516
          :|||||| |:|||||||||:|:|  |||| ||| |||||||:|| ::| |: |||:||
Db    412 IYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVT 470

Qy    517 SSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDTSDL 564
          ||||::|  :|||||||||:|   : :|   :|:::|| |||| ||| : |
Db    471 SSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 519


RESULT 4
US-09-724-676-84446
; Sequence 84446, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84446
;   LENGTH: 308
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676-84446

  Query Match             22.8%;  Score 682.5;  DB 5;  Length 308;
  Best Local Similarity   45.1%;  Pred. No. 1.2e-56;
  Matches  137;  Conservative   65;  Mismatches   85;  Indels   17;  Gaps    5;

Qy    271 KKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLK 330
          |::| |     :|   || |   |  | | ::  ::   | | : ::| |  |  :|
Db     13 KQISDLHKSLEQKESKIQQLAETIKKLEKEFKQFAQLFGKNGSFLPNIQ-VFASHIDKSA 71

Qy    331 ELDKEIRPF------RQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQL 384
           |: ::         :||  :   :  :|:::: ::| ||: |       :   :|| :
Db     72 WLEAQVHQLLQMVNQQQNKFDLRPLMEAVDTVKQKITLLENND-------QRLAVLEEET 124

Qy    385 SRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPF 444
          ::||  :::|  :|:  : ||::||   ||| |||| ||| :|:|||| | |:|::|| |
Db    125 NKHDTHINIHKAQLSKNEERFKLLEGTCYNGKLIWKVTDYKMKKREAVDGHTVSIFSQSF 184

Qy    445 YTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSR 504
          ||   ||:|||| |||||| |:|:|||||:||:||||:|:|| |||:|:|||||:|| | :
Db    185 YTSRCGYRLCARAYLNGDGSGRGSHLSLYFVVMRGEFDSLLQWPFRQRVTLMLLDQ-SGK 243

Qy    505 RHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTS 562
          ::: : |||||||||||:| |||||||||| ||| :||||    ||||||:|:|| || :
Db    244 KNIMETFKPDPNSSSFKRPDGEMNIASGCPRFVAHSVLENAKNAYIKDDTLFLKVAVDLT 303

Qy    563 DLPD 566
          || |
Db    304 DLED 307


RESULT 5
US-09-724-676A-84446
; Sequence 84446, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84446
;   LENGTH: 308
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676A-84446

  Query Match             22.8%;  Score 682.5;  DB 5;  Length 308;
  Best Local Similarity   45.1%;  Pred. No. 1.2e-56;
  Matches  137;  Conservative   65;  Mismatches   85;  Indels   17;  Gaps    5;

Qy    271 KKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLK 330
          |::| |     :|   || |   |  | | ::  ::   | | : ::| |  |  :|
Db     13 KQISDLHKSLEQKESKIQQLAETIKKLEKEFKQFAQLFGKNGSFLPNIQ-VFASHIDKSA 71

Qy    331 ELDKEIRPF------RQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQL 384
           |: ::         :||  :   :  :|:::: ::| ||: |       :   :|| :
Db     72 WLEAQVHQLLQMVNQQQNKFDLRPLMEAVDTVKQKITLLENND-------QRLAVLEEET 124

Qy    385 SRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPF 444
          ::||  :::|  :|:  : ||::||   ||| |||| ||| :|:|||| | |:|::|| |
Db    125 NKHDTHINIHKAQLSKNEERFKLLEGTCYNGKLIWKVTDYKMKKREAVDGHTVSIFSQSF 184

Qy    445 YTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSR 504
          ||   ||:|||| |||||| |:|:|||||:||:||||:|:|| |||:|:|||||:|| | :
Db    185 YTSRCGYRLCARAYLNGDGSGRGSHLSLYFVVMRGEFDSLLQWPFRQRVTLMLLDQ-SGK 243

Qy    505 RHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTS 562
          ::: : |||||||||||:| |||||||||| ||| :||||    ||||||:|:|| || :
Db    244 KNIMETFKPDPNSSSFKRPDGEMNIASGCPRFVAHSVLENAKNAYIKDDTLFLKVAVDLT 303

Qy    563 DLPD 566
          || |
Db    304 DLED 307


RESULT 6
US-09-724-676-53796
; Sequence 53796, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53796
;   LENGTH: 536
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676-53796

  Query Match             21.8%;  Score 652.5;  DB 5;  Length 536;
  Best Local Similarity   31.2%;  Pred. No. 1.8e-53;
  Matches  161;  Conservative   88;  Mismatches  170;  Indels   97;  Gaps   19;

Qy     62 PKQTECGHRFCESCMAALLSSSSPKCTAC-QESIIKDKV--------FKDNCCKREILAL 112
          | | :|||||:|  |:|:::|||    | ||  | | :: :        | ||  :: : :|
Db     62 PFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARKGVESL 121

Qy    113 QVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRAD---CKEKVLRKDLRDHVEKAC 169
            | ::  ||  : ||          |     | :  :   ||  |   :  |:|  |
Db    122 PAVCPSD--GCTWKGTLKEY-----ESCHEGRCPLMLTECPACKGLVRLGEKERHLEHEC 174

Qy    170 KYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS 229
            |  :| ||::      :: | :  ||   ::|   |  : : | :   |:  |
Db    175 PERSLSCRHCRAPCCGADVKAHHEV-CPKFPLTC-DGCGKKKIPREKFQDHVKTCGKCRV 232

Qy    230 TCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK----------VSLLQ 277
            | |   ||:   :|  ||   ||     :|: :|   |: || |           |||
Db    233 PCRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQ 288

Qy    278 N-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEI 336
            ||:||  :  :  | :|    |:||                   :   ||
Db    289 RCESLEKKTA--TFENIVCVLNREVER-----------------VAMTAEACS------ 322

Qy    337 RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDI 396
             ||:  : |     :|:| ::| :||                          ::: : |:
Db    323 ---RQHRLDQD----KIEALSSKVQQLE-----------------------RSIGLKDL 351
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Qy    397 RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR 456
          :||:: : :  :    :   : :    |: |||| |:  :::|  |||  :|||||  |
Db    352 AMADLEQKVRPFQAQCGHRYCSFCLASILRKLQEAVAGRIPAIFSPAFYTSRYGYKMCLR 411

Qy    457 VYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPN 516
          :|||||| |:|||||||||:|:|  |||| ||| |||||||:|| ::| |: |||:||
Db    412 IYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVT 470

Qy    517 SSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDD 551
          ||||::|  :|||||||||:|   : :|   :|::||
Db    471 SSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRDD 506


RESULT 7
US-09-724-676A-53796
; Sequence 53796, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53796
;   LENGTH: 536
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-676A-53796

  Query Match             21.8%;  Score 652.5;  DB 5;  Length 536;
  Best Local Similarity   31.2%;  Pred. No. 1.8e-53;
  Matches  161;  Conservative   88;  Mismatches  170;  Indels   97;  Gaps   19;

Qy     62 PKQTECGHRFCESCMAALLSSSSPKCTAC-QESIIKDKV--------FKDNCCKREILAL 112
          | | :|||||:|  |:|::|||    | ||  | | :: :        | ||  :: : :|
Db     62 PFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARKGVESL 121

Qy    113 QVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRAD---ČKEKVLRKDLRDHVEKAC 169
          |  ::  ||  : ||        |   | :  :   ||  |   :   |:|  |
Db    122 PAVCPSD--GCTWKGTLKEY-----ESCHEGRCPLMLTECPACKGLVRLGEKERHLEHEC 174

Qy    170 KYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS 229
            :| ||::      :: | :  ||   ::|   |  : : | :   |:  |
Db    175 PERSLSCRHCRAPCCGADVKAHHEV-CPKFPLTC-DGCGKKKIPREKFQDHVKTCGKCRV 232

Qy    230 TCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK----------VSLLQ 277
          | |   ||:   :|  ||   ||     :|: :|   |: || |            |||
Db    233 PCRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQ 288

Qy    278 N-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEI 336
            ||:||  :  :  | :|    |:||                :   ||
Db    289 RCESLEKKTA--TFENIVCVLNREVER-----------------VAMTAEACS------ 322

Qy    337 RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDI 396
            ||:  : |    :|:| ::| :||  .                  ::: : |:
Db    323 ---RQHRLDQD----KIEALSSKVQQLE----------------------RSIGLKDL 351

Qy    397 RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR 456
          :||:: : :  :    :   : :    |: |||| |:  :::|  |||  :|||||  |
Db    352 AMADLEQKVRPFQAQCGHRYCSFCLASILRKLQEAVAGRIPAIFSPAFYTSRYGYKMCLR 411

Qy    457 VYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPN 516
          :|||||| |:|||||||||:|:|  |||| ||| |||||||:|| ::| |: |||:||
Db    412 IYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVT 470

Qy    517 SSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDD 551
          ||||::|  :|||||||||:|   : :|   :|::||
Db    471 SSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRDD 506


RESULT 8
US-10-283-500-2
```

```
; Sequence 2, Application US/10283500
;  GENERAL INFORMATION:
;       APPLICANT: Goeddel, David V.
;                  Rothe. Mike
;       TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
;       NUMBER OF SEQUENCES: 59
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/283,500
;            FILING DATE: 30-Oct-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/779,599
;            FILING DATE: 07-Jan-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger R.
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: P0897C2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-3216
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 409 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-283-500-2

  Query Match             21.4%;  Score 640;  DB 6;  Length 409;
  Best Local Similarity   35.5%;  Pred. No. 1.9e-52;
  Matches  162;  Conservative   72;  Mismatches  136;  Indels   86;  Gaps   15;

Qy    137 KNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDC 196
          :|| ||    |  | |::              : |   |: | |:     |:  ||  |
Db      9 ENEFQF---GCPPAPCQD------------PSEPRVLCCTACLSE----NLRDDEDRIC 48

Qy    197 PCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAV 256
          |       |  | : | |   | |:   |   | |   || |:|: | :: |||:|
Db     49 PKCRADNLHPVSPGSPLTQE-KVH-SDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQS 106

Qy    257 QHVNL----LKEWSNS----------LEKKVSLLQNESVEKNKSIQSLHNQICSFEIEI 301
          |: |    |||| :|           ||: :| ||         :|:        |::
Db    107 SHLYLLLAVLKEWKSSPGSNLGSAPMALERNLSELQ---------LQAAVEATGDLEVDC 157

Qy    302 ERQKEMLRNNESKILHLQRVIDSQAEK-LKELDKEIRPFRQNWEEADSMKSSVESLQNRV 360
          |     |  : || :      || | :|::::| |           ::: :: |:
Db    158 YRAPCCESQEELALQHLVK------EKLLAQLEEKLRVF----------ANIVAVLNKE 200

Qy    361 TELESVDKSAGQAARNTGLLESQLSRH-----------DQTLSVHDIRLADMDLRFQVL 408
          |       |   |    : :||| |              |||:  |  |  ::   :::
Db    201 VE-------ASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLM 253

Qy    409 ETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 468
          | ||::|  :||| :  :|  |:| |:|:||:|  |||  :|||:| |:|||||  || |
Db    254 EEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRLYLNGDGSGKKT 313

Qy    469 HLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMN 528
          ||||| ||||||||||||||: ||| ||:|| ::| |  |||:|| :|:||::|  | |
Db    314 HLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQ-NNREHAIDAFRPDLSSASFQRPQSETN 372
```

```
Qy    529 IASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTS 562
          :|||||:|   : |::    |:||||:|:| |||||
Db    373 VASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVDTS 408


RESULT 9
US-60-423-586-89
; Sequence 89, Application US/60423586
; GENERAL INFORMATION:
;  APPLICANT: American Home Products Inc.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING SCHIZOPHRENI
;  FILE REFERENCE: AM101288L
;  CURRENT APPLICATION NUMBER: US/60/423,586
;  CURRENT FILING DATE:  2002-11-05
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-423-586-89

  Query Match             18.7%;  Score 560.5;  DB 7;  Length 470;
  Best Local Similarity   24.1%;  Pred. No. 7.7e-45;
  Matches  142;  Conservative   81;  Mismatches  173;  Indels  193;  Gaps   12;

Qy     37 GYKEKFVKTVEDKYKCEKCRLVLCNPKQ-TECGHRFCESCMAALLSSSSPKCTACQESII 95
          |:  ||::  : :  |  |   :  | | : ||||||::|:   ||    ||   | :
Db      3 GFDYKFLEKPKRRLLCPLCGKPMREPVQVSTCGHRFCDTCLQEFLSEGVFKCPEDQLPLD 62

Qy     96 KDKVFKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPC-------- 147
            |:: |   : ::| | : | :   ||     | ||  || | | |  :||
Db     63 YAKIYPDPELEVQVLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPCPNRCPMKL 121

Qy    148 --------LRADCKE-------------------------------------KVLRKDLR 162
                 |: || :                                      :::|: |
Db    122 SRRDLPAHLQHDCPKRRLKCEFCGCDFSGEAYESHEGMCPQESVYCENKCGARMMRRLLA 181

Qy    163 DHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLS 222
          |    |  |   |::|  :     :| |:   || : |:||::| | |: | :|  ||
Db    182 QHATSECPKRTQPCTYCTKEFVFDTIQSHQ-YQCPRLPVACPNQCGVGTVAREDLPGHLK 240

Qy    223 E-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESV 281
          : |  |   | ||  ||  :    :  |   |   |: ::
Db    241 DSCNTALVLCPFKDSGCKHRCPKLAMARHVEESVKPHLAMM------------------- 281

Qy    282 EKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQ 341
                      |:                    ::  | ::|:|| :|:
Db    282 ------------CA----------------------LVSRQRQELQELRREL----- 299

Qy    342 NWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADM 401
                                                  : |||
Db    300 ------------------------------------------------EELSV-------- 304

Qy    402 DLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNG 461
                    :|||||||  | || |||     |  :|  |||  :|||:    :|||
Db    305 ----------GSDGVLIWKIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSAFLNG 354

Qy    462 DGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPNS 517
          :| |:||||||:  :: | :| || ||| ::||  |:||     :  :|: : | ||||
Db    355 NGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPNW 414

Qy    518 SSFKKP------TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD 560
           :|:||       | ::  | | |::   :    |::|| :||:  |:
Db    415 KNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE 463


RESULT 10
US-60-427-194-89
; Sequence 89, Application US/60427194
; GENERAL INFORMATION:
;  APPLICANT: American Home Products Inc.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING SCHIZOPHRENI
;  FILE REFERENCE: AM101228L
;  CURRENT APPLICATION NUMBER: US/60/427,194
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-427-194-89

  Query Match             18.7%;  Score 560.5;  DB 7;  Length 470;
  Best Local Similarity   24.1%;  Pred. No. 7.7e-45;
  Matches  142;  Conservative   81;  Mismatches  173;  Indels  193;  Gaps   12;

Qy     37 GYKEKFVKTVEDKYKCEKCRLVLCNPKQ-TECGHRFCESCMAALLSSSSPKCTACQESII 95
          |:  ||::  : :  |  |   :  | | : ||||||::|:   ||    ||   | :
Db      3 GFDYKFLEKPKRRLLCPLCGKPMREPVQVSTCGHRFCDTCLQEFLSEGVFKCPEDQLPLD 62

Qy     96 KDKVFKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPC-------- 147
            |:: |   : ::| | : | :   ||     | ||  || | | |  :||
Db     63 YAKIYPDPELEVQVLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPCPNRCPMKL 121

Qy    148 --------LRADCKE-------------------------------------KVLRKDLR 162
                 |: || :                                      :::|: |
Db    122 SRRDLPAHLQHDCPKRRLKCEFCGCDFSGEAYESHEGMCPQESVYCENKCGARMMRRLLA 181

Qy    163 DHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLS 222
          |    |  |   |::|  :     :| |:   || : |:||::| | |: | :|  ||
Db    182 QHATSECPKRTQPCTYCTKEFVFDTIQSHQ-YQCPRLPVACPNQCGVGTVAREDLPGHLK 240

Qy    223 E-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESV 281
          : |  |   | ||  ||  :    :  |   |   |: ::
Db    241 DSCNTALVLCPFKDSGCKHRCPKLAMARHVEESVKPHLAMM------------------- 281

Qy    282 EKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQ 341
                      |:                    ::  | ::|:|| :|:
Db    282 ------------CA----------------------LVSRQRQELQELRREL----- 299

Qy    342 NWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADM 401
                                                  : |||
Db    300 ------------------------------------------------EELSV-------- 304

Qy    402 DLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNG 461
                    :|||||||  | || |||     |  :|  |||  :|||:    :|||
Db    305 ----------GSDGVLIWKIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSAFLNG 354

Qy    462 DGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPNS 517
          :| |:||||||:  :: | :| || ||| ::||  |:||     :  :|: : | ||||
Db    355 NGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPNW 414

Qy    518 SSFKKP------TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD 560
           :|:||       | ::  | | |::   :    |::|| :||:  |:
Db    415 KNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE 463


RESULT 11
US-09-716-536-10
; Sequence 10, Application US/09716536
; GENERAL INFORMATION:
;  APPLICANT: Soo Young Lee
;  APPLICANT:  Yongwon Choi
;  TITLE OF INVENTION: Signal Transducer for the TNF Receptor
;  TITLE OF INVENTION:  Super Family and Uses Thereof
;  FILE REFERENCE: 600-1-198CIP1CON
;  CURRENT APPLICATION NUMBER: US/09/716,536
;  CURRENT FILING DATE:  2000-11-20
;  PRIOR APPLICATION NUMBER: 60/042,293
;  PRIOR FILING DATE: 1997-04-01
;  PRIOR APPLICATION NUMBER: 60/042,747
;  PRIOR FILING DATE: 1997-04-07
;  PRIOR APPLICATION NUMBER: 08/834,903
;  PRIOR FILING DATE: 1997-04-07
```

```
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 46
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fragment
US-09-716-536-10

  Query Match             8.7%;  Score 259;  DB 5;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-17;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      49 KYKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESI 94
           |||||||||||||||||||||||||||||||||||||||||||||
Db       1 KYKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESI 46


RESULT 12
US-10-197-666A-120
; Sequence 120, Application US/10197666A
; GENERAL INFORMATION:
;  APPLICANT: ASAHI KASEI KABUSIKI KAISYA
;  TITLE OF INVENTION: Elk1 phosphorylation related gene
;  FILE REFERENCE: PH-1548US
;  CURRENT APPLICATION NUMBER: US/10/197,666A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: JP 2001-218204
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: JP 2001-263450
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: JP 2002-012176
;  PRIOR FILING DATE: 2002-01-21
;  PRIOR APPLICATION NUMBER: US 60/305,884
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/316,304
;  PRIOR FILING DATE: 2001-09-04
;  PRIOR APPLICATION NUMBER: US 60/350,027
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-197-666A-120

  Query Match             6.9%;  Score 205.5;  DB 6;  Length 600;
  Best Local Similarity   21.3%;  Pred. No. 4.8e-11;
  Matches  102;  Conservative   50;  Mismatches  165;  Indels  161;  Gaps   19;

Qy      10 AGTLQPNPPLKLQPDRGAGSVL-------VPEQGGYKEKFVKTVEDKYK--CEKCRLVLC 60
           || | |  || ::      : :       :||:    |  |   :   |  |: |  |
Db      10 AGHLPPLAPLPIRHGMRRTACMSLRSTFSLPEEEEEPEPLVFAEQPSVKLCCQLCCSVFK 69

Qy      61 NPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVYCRNEG 120
           :|  | ||| ||  |     :  | ||                ||          | |   |
Db      70 DPVITTCGHTFCRRC-----ALKSEKCPV-----------DNA------KLTVVVNN-- 104

Qy     121 RGCAEQLTLGHLLVHLKNECQ---------FEELPCLRADCKEKVLRKDLRDHVEKACKY 171
              |||  :| | :| :: |           ||  |     |   :     :|| | :| |
Db     105 IAVAEQ--IGELFIHCRHGCHAAGTGKPGVFEVDP---RGCPFTIKLSARKDH-ESSCDY 158

Qy     172 REATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTC 231
           |                            | ||:  |   ||:  | ||| || :    |
Db     159 RP--------------------------VRCPNNPSCPPLLKMNLEAHLKECEHI--KC 189

Qy     232 SFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLH 291
           :||| | |                                              |:     |
Db     190 PHSKYGCTFIG-----------------------------------------NQDTYETH 208

Qy     292 NQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKS 351
           : | |    |  || |:  : :  |   |       | : |:||           ::|
Db     209 LETCRF----EGLKEFLQQTDDR-FHEMHV------ALAQKDQEIA----------FLRS 247

Qy     352 SVESLQNRVTELE-SVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLET 410
           :  |  :: :|| |::         |   |   |    :  |: :  |: :: |  :
Db     248 MLGKLSEKIDQLEKSLELKFDVLDENQSKLSEDLMEFRRDASMLNDELSHINARLNMGIL 307

Qy     411 ASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 468
           ||:   |:| :                    : |: |   |  ||  || :  |:
Db     308 GSYDPQQIFKCKG-------------------TFVGHQGPVWCLCVYSMGDLLFSGS 345


RESULT 13
US-10-197-666A-112
; Sequence 112, Application US/10197666A
; GENERAL INFORMATION:
;  APPLICANT: ASAHI KASEI KABUSIKI KAISYA
;  TITLE OF INVENTION: Elk1 phosphorylation related gene
;  FILE REFERENCE: PH-1548US
;  CURRENT APPLICATION NUMBER: US/10/197,666A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: JP 2001-218204
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: JP 2001-263450
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: JP 2002-012176
;  PRIOR FILING DATE: 2002-01-21
;  PRIOR APPLICATION NUMBER: US 60/305,884
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/316,304
;  PRIOR FILING DATE: 2001-09-04
;  PRIOR APPLICATION NUMBER: US 60/350,027
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;   LENGTH: 641
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-197-666A-112

  Query Match             6.8%;  Score 203;  DB 6;  Length 641;
  Best Local Similarity   21.5%;  Pred. No. 9.1e-11;
  Matches   96;  Conservative   48;  Mismatches  154;  Indels  148;  Gaps   18;

Qy      32 VPEQGGYKEKFVKTVEDKYK--CEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTA 89
           :||:    |  |   :   |  |: |  |  :|  | |||  ||  |     :  | ||
Db      80 LPEEEEEPEPLVFAEQPSVKLCCQLCCSVFKDPVITTCGHTFCRRC-----ALKSEKCPV 134

Qy      90 CQESIIKDKVFKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFE---ELP 146
                   ||       : | |    |      ||| , :| | :| :: |:      : |
Db     135 ------------DN------VKLTVVVNN--IAVAEQ--IGELFIHCRHGCRVAGSGKPP 172

Qy     147 CLRAD---CKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSC 203
               |   |   :     :|| | :| ||                          | |
Db     173 IFEVDPRGCPFTIKLSARKDH-EGSCDYRP--------------------------VRC 204

Qy     204 PHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLK 263
           |:  |   |||  | ||| || :    |   :||| | |
Db     205 PNNPSCPPLLRMNLEAHLKECEHI--KCPHSKYGCTFIG---------------------- 241

Qy     264 EWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVID 323
                         |:     | : | |    |  || |:  : :  |   |
Db     242 --------------------NQDTYETHLETCRF----EGLKEFLQQTDDR-FHEMHV-- 274

Qy     324 SQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELE-SVDKSAGQAARNTGLLES 382
           |  : |:||            ::| :  |  :: :|| |::         |   |
Db     275 ----ALAQKDQEIA----------FLRSMLGKLSEKIDQLEKSLELKFDVLDENQSKLSE 320

Qy     383 QLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQ 442
           |    :  |: :  |: :: |  :    ||:   |:| :
Db     321 DLMEFRRDASMLNDELSHINARLNMGILGSYDPQQIFKCKG---------------------- 361
```

```
Qy     443 PFYTGYFGYKMCARVYLNGDGMGKGT 468
           : |: |   |  ||  || :  |:
Db     362 -TFVGHQGPVWCLCVYSMGDLLFSGS 386


RESULT 14
US-10-197-666A-150
; Sequence 150, Application US/10197666A
; GENERAL INFORMATION:
;  APPLICANT: ASAHI KASEI KABUSIKI KAISYA
;  TITLE OF INVENTION: Elk1 phosphorylation related gene
;  FILE REFERENCE: PH-1548US
;  CURRENT APPLICATION NUMBER: US/10/197,666A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: JP 2001-218204
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: JP 2001-263450
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: JP 2002-012176
;  PRIOR FILING DATE: 2002-01-21
;  PRIOR APPLICATION NUMBER: US 60/305,884
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/316,304
;  PRIOR FILING DATE: 2001-09-04
;  PRIOR APPLICATION NUMBER: US 60/350,027
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
;   LENGTH: 670
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-197-666A-150

  Query Match             6.8%;  Score 203;  DB 6;  Length 670;
  Best Local Similarity   21.5%;  Pred. No. 9.7e-11;
  Matches   96;  Conservative   48;  Mismatches  154;  Indels  148;  Gaps   18;

Qy      32 VPEQGGYKEKFVKTVEDKYK--CEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTA 89
           :||:    |  |   :   |  |: |  |  :|  | ||| ||  |      :  | ||
Db     109 LPEEEEEPEPLVFAEQPSVKLCCQLCCSVFKDPVITTCGHTFCRRC-----ALKSEKCPV 163

Qy      90 CQESIIKDKVFKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFE---ELP 146
                   ||      : | |   |      |||  :| | :| :: |:     : |
Db     164 -----------DN------VKLTVVVNN--IAVAEQ--IGELFIHCRHGCRVAGSGKPP 201

Qy     147 CLRAD---CKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSC 203
           |   |   :     :|| | :| ||                          | |
Db     202 IFEVDPRGCPFTIKLSARKDH-EGSCDYRP-------------------------VRC 233

Qy     204 PHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLK 263
           |:  |   |||  | ||| || :    |   :||| | |
Db     234 PNNPSCPPLLRMNLEAHLKECEHI--KCPHSKYGCTFIG---------------------- 270

Qy     264 EWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVID 323
                       |:     | : | |    |  || |:  : :  |   |
Db     271 -------------------NQDTYETHLETCRF----EGLKEFLQQTDDR-FHEMHV-- 303

Qy     324 SQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELE-SVDKSAGQAARNTGLLES 382
           | : |:||            ::| :  |  :: :|| |::       |   |
Db     304 ----ALAQKDQEIA----------FLRSMLGKLSEKIDQLEKSLELKFDVLDENQSKLSE 349

Qy     383 QLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQ 442
           |    :  |: :  |: :: |  :    ||:   |:| :
Db     350 DLMEFRRDASMLNDELSHINARLNMGILGSYDPQQIFKCKG------------------ 390

Qy     443 PFYTGYFGYKMCARVYLNGDGMGKGT 468
           : |: |   |  ||  || :  |:
Db     391 -TFVGHQGPVWCLCVYSMGDLLFSGS 415


RESULT 15
US-10-197-666A-116
; Sequence 116, Application US/10197666A
; GENERAL INFORMATION:
;  APPLICANT: ASAHI KASEI KABUSIKI KAISYA
;  TITLE OF INVENTION: Elk1 phosphorylation related gene
;  FILE REFERENCE: PH-1548US
;  CURRENT APPLICATION NUMBER: US/10/197,666A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: JP 2001-218204
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: JP 2001-263450
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: JP 2002-012176
;  PRIOR FILING DATE: 2002-01-21
;  PRIOR APPLICATION NUMBER: US 60/305,884
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/316,304
;  PRIOR FILING DATE: 2001-09-04
;  PRIOR APPLICATION NUMBER: US 60/350,027
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
;   LENGTH: 631
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-197-666A-116

  Query Match             6.7%;  Score 202;  DB 6;  Length 631;
  Best Local Similarity   21.3%;  Pred. No. 1.1e-10;
  Matches  101;  Conservative   48;  Mismatches  174;  Indels  152;  Gaps   17;

Qy       4 SKKMDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKTVEDKYKCEKCRLVLCNPK 63
           :|  |  || : :           | |    | |      | :   |  |: |  |  :|
Db      44 TKAADGTGTYKQHRRTPSSSSTLAYSPRDEEDGMEPLVFAEQPSVKLCCQLCCSVFKDPV 103

Qy      64 QTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVYCRNEGRGC 123
           | ||| ||  |      :  | ||                ||        | |   |
Db     104 ITTCGHTFCRRC-----ALKSEKCPV-----------DNA------KLTVVVNN--IAV 138

Qy     124 AEQLTLGHLLVHLKNECQ---------FEELPCLRADCKEKVLRKDLRDHVEKACKYREA 174
           |||  :| | :| :: |             ||  |     |   :     :|| | :| ||
Db     139 AEQ--IGELFIHCRHGCHAAGTGKPGVFEVDP---RGCPFTIKLSARKDH-ESSCDYRP- 191

Qy     175 TCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFK 234
                                       | ||:  |   ||:  | ||| || :    |
Db     192 -------------------------VRCPNNPSCPPLLKMNLEAHLKECEHI--KCPHS 223

Qy     235 RYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQI 294
           :||| | |                                          |:     | :
Db     224 KYGCTFIG-----------------------------------------NQDTYETHLET 242

Qy     295 CSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVE 354
           | |    |  || |: :: :  |  |        | : |:||           ::| :
Db     243 CRF----EGLKEFLQQSDDR-FHEMHV------ALAQKDQEIA----------FLRSMLG 281

Qy     355 SLQNRVTELE-SVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASY 413
           |  :: :|| |::          |   |    |    :  |: :  |: :: |  :    ||
Db     282 KLSEKINQLEKSLELKFDVLDENQSKLSEDLMEFRRDASMLNDELSHINARLNMGILGSY 341

Qy     414 NGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 468
           :   |:| :                    : |: |   |  ||  || :  |:
Db     342 DPQQIFKCKG-------------------TFVGHQGPVWCLCVYSMGDLLFSGS 376


Search completed: December 19, 2002, 15:05:20
Job time : 21 secs
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